Amendments to the Specification:

Please replace the paragraph beginning at page 11, line ~~31~~ 12 as with the following amended paragraph:

~~Figure 1~~Figures 1A and 1B ~~depicts~~ depict a proposed biosynthetic pathway for BL. CR goes through at least two different pathways, referred to as the early C-6 oxidation (right column) and late C-6 oxidation (left column) pathways. Steps mediated by DWF4, CPD (Szerkeres et al. (1996), *supra*), DET2 (Fujioka and Skaurai (1997a), *infra*; Li et al. (1997), *supra*) and LKB (Yokota et al. (1997), *infra*) are indicated.

Please replace the paragraph beginning at page 11, line 31 as with the following amended paragraph:

~~Figure 3~~Figures 3A and 3B ~~depicts~~ depict an alignment of cytochrome P450 proteins that exhibited the most similarity to DWF4 (SEQ. ID NO:2) in BLAST searches. GenBank accession numbers are AF044216 (DWF4; CYP90B) (SEQ. ID NO:2), X87368 (CPD; CYP90A), U54770 (tomato; CYP85), D64003 (cyanobacteria; CYP120), U32579 (maize; CYP88), U68234 (zebrafish; CYP26), and M13785 (human; CYP3A3X). Dashes indicate gaps introduced to maximize alignment. Domains indicated in Figure 2B are highlighted in a box. Amino acid residues that are conserved >50% between the compared sequences are highlighted by a reverse font, and identical residues between DWF4 and CPD are boxed and italicized. Open triangles are placed under the 100% conserved residues. Closed triangles locate functionally important amino acid residues, for example, threonine (T) at 369, which is thought to bind molecular oxygen, and cysteine (C) at 516, which links to a heme prosthetic group by a thiolate bond. X's indicate mutated residues in *dwf4* alleles. Multiple sequence alignment was performed using PILEUP in the Genetics Computer Group package, and box shading was made possible by the ALSCRIPT package (Barton (1993) *Protein Eng.* 6:37-40).

Please replace the paragraph beginning at page 13, line 24 as with the following amended paragraph: